

OHDD
#2

0520/0420



OIQE

RAW SEQUENCE LISTING

DATE: 02/16/2002

PATENT APPLICATION: US/10/068,080

TIME: 13:17:21

Input Set : N:\Crf3\RULE60\10068080.txt

Output Set: N:\CRF3\02152002\J068080.raw

4 <110> APPLICANT: Fritz, Christian
 5 Youngman, Philip
 7 <120> TITLE OF INVENTION: USE OF YNES, ESSENTIAL BACTERIAL GENES AND POLYPEPTIDES
 9 <130> FILE REFERENCE: 07334/090001
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/068,080
 12 <141> CURRENT FILING DATE: 2002-02-05
 W--> 14 <140> CURRENT APPLICATION NUMBER: US 09/163,445
 15 <141> CURRENT FILING DATE: 1998-09-30
 18 <150> PRIOR APPLICATION NUMBER: US 60/070,116
 19 <151> PRIOR FILING DATE: 1997-12-31
 21 <160> NUMBER OF SEQ ID NOS: 12
 23 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 213
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Streptococcus pneumoniae
 30 <400> SEQUENCE: 1
 31 Met Ile Thr Ile Val Leu Leu Ile Leu Ala Tyr Leu Leu Gly Ser Ile
 32 1 5 10 15
 33 Pro Ser Gly Leu Trp Ile Gly Gln Val Phe Phe Gln Ile Asn Leu Arg
 34 20 25 30
 35 Glu His Gly Ser Gly Asn Thr Gly Thr Thr Asn Thr Phe Arg Ile Leu
 36 35 40 45
 37 Gly Lys Lys Ala Gly Met Ala Thr Phe Val Ile Asp Phe Phe Lys Gly
 38 50 55 60
 39 Thr Leu Ala Thr Leu Leu Pro Ile Ile Phe His Leu Gln Gly Val Ser
 40 65 70 75 80
 41 Pro Leu Ile Phe Gly Leu Leu Ala Val Ile Gly His Thr Phe Pro Ile
 42 85 90 95
 43 Phe Ala Gly Phe Lys Gly Gly Lys Ala Val Ala Thr Ser Ala Gly Val
 44 100 105 110
 45 Ile Phe Gly Phe Ala Pro Ile Phe Cys Leu Tyr Leu Ala Ile Ile Phe
 46 115 120 125
 47 Phe Gly Ala Leu Tyr Leu Gly Ser Met Ile Ser Leu Ser Ser Val Thr
 48 130 135 140
 49 Ala Ser Ile Ala Ala Val Ile Gly Val Leu Leu Phe Pro Leu Phe Gly
 50 145 150 155 160
 51 Phe Ile Leu Ser Asn Tyr Asp Ser Leu Phe Ile Ala Ile Ile Leu Ala
 52 165 170 175
 53 Leu Ala Ser Leu Ile Ile Ile Arg His Lys Asp Asn Ile Ala Arg Ile
 54 180 185 190
 55 Lys Asn Lys Thr Glu Asn Leu Val Pro Trp Gly Leu Asn Leu Thr His
 56 195 200 205

ENTERED

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57 Gln Asp Pro Lys Lys
58      210
60 <210> SEQ ID NO: 2
61 <211> LENGTH: 642
62 <212> TYPE: DNA
63 <213> ORGANISM: Streptococcus pneumoniae
65 <220> FEATURE:
66 <221> NAME/KEY: CDS
67 <222> LOCATION: (1)...(639)
71 <400> SEQUENCE: 2
72 atg att aca ata gtt tta tta atc cta gcc tat ctg ctg ggt tcg att      48
73 Met Ile Thr Ile Val Leu Leu Ile Leu Ala Tyr Leu Leu Gly Ser Ile
74      1      5      10      15
76 cca tct ggt ctc tgg att gga caa gta ttc ttt caa atc aat cta cgc      96
77 Pro Ser Gly Leu Trp Ile Gly Gln Val Phe Phe Gln Ile Asn Leu Arg
78      20      25      30
80 gag cat ggt tct ggt aac act gga acg acc aac acc ttc cgc att tta      144
81 Glu His Gly Ser Gly Asn Thr Gly Thr Thr Asn Thr Phe Arg Ile Leu
82      35      40      45
84 ggt aag aaa gct ggt atg gca acc ttt gtg att gac ttt ttc aaa gga      192
85 Gly Lys Lys Ala Gly Met Ala Thr Phe Val Ile Asp Phe Phe Lys Gly
86      50      55      60
88 acc cta gca acg ctg ctt ccg att att ttt cat cta caa ggc gtt tct      240
89 Thr Leu Ala Thr Leu Leu Pro Ile Ile Phe His Leu Gln Gly Val Ser
90      65      70      75      80
92 cct ctc atc ttt gga ctt ttg gct gtt atc ggc cat acc ttc cct atc      288
93 Pro Leu Ile Phe Gly Leu Leu Ala Val Ile Gly His Thr Phe Pro Ile
94      85      90      95
96 ttt gca gga ttt aaa ggt ggt aag gct gtc gca acc agt gct gga gtg      336
97 Phe Ala Gly Phe Lys Gly Gly Lys Ala Val Ala Thr Ser Ala Gly Val
98      100      105      110
100 att ttc gga ttt gcg cct atc ttc tgt ctc tac ctt gcg att atc ttc      384
101 Ile Phe Gly Phe Ala Pro Ile Phe Cys Leu Tyr Leu Ala Ile Ile Phe
102      115      120      125
104 ttt gga gct ctc tat ctt ggc agt atg att tca ctg tct agt gtc aca      432
105 Phe Gly Ala Leu Tyr Leu Gly Ser Met Ile Ser Leu Ser Ser Val Thr
106      130      135      140
108 gca tcg att gcg gct gtt atc ggg gtt ctg ctc ttt cca ctt ttt ggt      480
109 Ala Ser Ile Ala Ala Val Ile Gly Val Leu Leu Phe Pro Leu Phe Gly
110      145      150      155      160
112 ttt atc ctg agt aac tat gac tct ctc ttc atc gct att atc tta gca      528
113 Phe Ile Leu Ser Asn Tyr Asp Ser Leu Phe Ile Ala Ile Ile Leu Ala
114      165      170      175
116 ctt gct agt ttg att atc att cgt cat aag gac aat ata gct cgt atc      576
117 Leu Ala Ser Leu Ile Ile Ile Arg His Lys Asp Asn Ile Ala Arg Ile
118      180      185      190
120 aaa aat aaa act gaa aat ttg gtc cct tgg gga ttg aac cta acc cat      624
121 Lys Asn Lys Thr Glu Asn Leu Val Pro Trp Gly Leu Asn Leu Thr His
122      195      200      205

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```

124  caa gat cct aaa aaa taa                                     642
125  Gln Asp Pro Lys Lys
126      210
128 <210> SEQ ID NO: 3
129 <211> LENGTH: 193
130 <212> TYPE: PRT
131 <213> ORGANISM: Streptococcus pneumoniae
135 <400> SEQUENCE: 3
136  Met Leu Ile Ala Leu Leu Ile Ile Leu Ala Tyr Leu Ile Gly Ser Ile
137      1          5          10          15
138  Pro Ser Gly Leu Ile Val Gly Lys Leu Ala Lys Gly Ile Asp Ile Arg
139      20          25          30
140  Glu His Gly Ser Gly Asn Leu Gly Ala Thr Asn Ala Phe Arg Thr Leu
141      35          40          45
142  Gly Val Lys Ala Gly Ser Val Val Ile Ala Gly Asp Ile Leu Lys Gly
143      50          55          60
144  Thr Leu Ala Thr Ala Leu Pro Phe Leu Met His Val Asp Ile His Pro
145      65          70          75          80
146  Leu Leu Ala Gly Val Phe Ala Val Leu Gly His Val Phe Pro Ile Phe
147      85          90          95
148  Ala Lys Phe Lys Gly Gly Lys Ala Val Ala Thr Ser Gly Gly Val Leu
149      100         105         110
150  Leu Phe Tyr Ala Pro Leu Leu Phe Ile Thr Met Val Ala Val Phe Phe
151      115         120         125
152  Ile Phe Leu Tyr Leu Thr Lys Phe Val Ser Leu Ser Ser Met Leu Thr
153      130         135         140
154  Gly Ile Tyr Thr Val Ile Tyr Ser Phe Phe Val His Asp Thr Tyr Leu
155      145         150         155         160
156  Leu Ile Val Val Thr Leu Leu Thr Ile Phe Val Ile Tyr Arg His Arg
157      165         170         175
158  Ala Asn Ile Lys Arg Ile Ile Asn Lys Thr Glu Pro Lys Val Lys Trp
159      180         185         190
160  Leu
163 <210> SEQ ID NO: 4
164 <211> LENGTH: 582
165 <212> TYPE: DNA
166 <213> ORGANISM: Streptococcus pneumoniae
168 <220> FEATURE:
169 <221> NAME/KEY: CDS
170 <222> LOCATION: (1)...(579)
172 <400> SEQUENCE: 4
173  atg tta att gct tta ttg att att ttg gcc tac ttg ata ggc agc att         48
174  Met Leu Ile Ala Leu Leu Ile Ile Leu Ala Tyr Leu Ile Gly Ser Ile
175      1          5          10          15
177  cca tct ggc tta att gtg ggc aag ctt gcc aaa gga att gat att cgg         96
178  Pro Ser Gly Leu Ile Val Gly Lys Leu Ala Lys Gly Ile Asp Ile Arg
179      20          25          30
181  gag cac gga agc ggc aac tta ggc gct acc aat gca ttc cgt aca ttg         144
182  Glu His Gly Ser Gly Asn Leu Gly Ala Thr Asn Ala Phe Arg Thr Leu

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```

183          35          40          45
185 ggt gta aaa gct ggt tcg gtc gtc ata gcc gga gat att ttg aaa ggg      192
186 Gly Val Lys Ala Gly Ser Val Val Ile Ala Gly Asp Ile Leu Lys Gly
187          50          55          60
189 aca ctg gca act gca ttg cct ttt ctc atg cat gtt gat att cac ccg      240
190 Thr Leu Ala Thr Ala Leu Pro Phe Leu Met His Val Asp Ile His Pro
191 65          70          75          80
193 ctt ctt gca gga gtc ttt gcg gtt tta ggc cac gtg ttt ccc atc ttc      288
194 Leu Leu Ala Gly Val Phe Ala Val Leu Gly His Val Phe Pro Ile Phe
195          85          90          95
199 gcc aaa ttt aaa ggc ggt aaa gcc gtg gcg aca tca gga ggc gtt ttg      336
200 Ala Lys Phe Lys Gly Gly Lys Ala Val Ala Thr Ser Gly Gly Val Leu
201          100          105          110
203 cta ttt tac gca ccc ctg tta ttt atc acg atg gtt gcg gta ttc ttc      384
204 Leu Phe Tyr Ala Pro Leu Leu Phe Ile Thr Met Val Ala Val Phe Phe
205          115          120          125
207 atc ttt tta tac ttg act aaa ttt gtt tct ctc tca tcg atg tta aca      432
208 Ile Phe Leu Tyr Leu Thr Lys Phe Val Ser Leu Ser Ser Met Leu Thr
209          130          135          140
211 ggg atc tat act gtt ata tat agt ttc ttt gtc cat gat acg tat tta      480
212 Gly Ile Tyr Thr Val Ile Tyr Ser Phe Phe Val His Asp Thr Tyr Leu
213          145          150          155          160
215 ttg att gtc gtt acc ctg ctc act att ttt gtg ata tac aga cac cga      528
216 Leu Ile Val Val Thr Leu Leu Thr Ile Phe Val Ile Tyr Arg His Arg
217          165          170          175
219 gcg aac att aaa cga att atc aat aaa aca gaa cct aaa gta aaa tgg      576
220 Ala Asn Ile Lys Arg Ile Ile Asn Lys Thr Glu Pro Lys Val Lys Trp
221          180          185          190
223 tta taa      582
224 Leu
227 <210> SEQ ID NO: 5
228 <211> LENGTH: 21
229 <212> TYPE: DNA
230 <213> ORGANISM: B. subtilis
232 <400> SEQUENCE: 5
233 gtgttcgtgc tgacttgcac c      21
235 <210> SEQ ID NO: 6
236 <211> LENGTH: 21
237 <212> TYPE: DNA
238 <213> ORGANISM: B. subtilis
240 <400> SEQUENCE: 6
241 gaattatttc ctcccgttaa a      21
243 <210> SEQ ID NO: 7
244 <211> LENGTH: 21
245 <212> TYPE: DNA
246 <213> ORGANISM: Steptococcus pneumoniae
248 <400> SEQUENCE: 7
249 acccactccg tgaagtccac c      21
251 <210> SEQ ID NO: 8

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252 <211> LENGTH: 21
253 <212> TYPE: DNA
254 <213> ORGANISM: Streptococcus pneumoniae
256 <400> SEQUENCE: 8
257   gaacccagca gataggctag g                                     21
259 <210> SEQ ID NO: 9
260 <211> LENGTH: 21
263 <212> TYPE: DNA
264 <213> ORGANISM: Streptococcus pneumoniae
266 <400> SEQUENCE: 9
267   gaacctaacc catcaagatc c                                     21
269 <210> SEQ ID NO: 10
270 <211> LENGTH: 24
271 <212> TYPE: DNA
272 <213> ORGANISM: Streptococcus pneumoniae
274 <400> SEQUENCE: 10
275   cagttttaga tggctttaac agcg                                   24
277 <210> SEQ ID NO: 11
278 <211> LENGTH: 642
279 <212> TYPE: DNA
280 <213> ORGANISM: Streptococcus pneumoniae
282 <400> SEQUENCE: 11
283   tactaatgtt atcaaaataa ttaggatcgg atagacgacc caagctaagg tagaccagag      60
284   acctaacctg ttcataagaa agtttagtta gatgcgctcg taccaagacc attgtgacct      120
285   tgctggttgt ggaaggcgta aaatccattc tttcgacct accgttgga acactaactg      180
286   aaaaagtttc cttgggatcg ttgcgacgaa ggctaataaa aagtagatgt tccgcaaaga      240
287   ggagagtaga aacctgaaaa ccgacaatag ccggtatgga agggatagaa acgtcctaaa      300
288   tttccaccat tccgacagcg ttggtcacga cctcactaaa agcctaaacg cggatagaag      360
289   acagagatgg aacgctaata gaagaaacct cgagagatag aaccgtcata ctaaagtgcac      420
290   agatcacagt gtcgtagcta acgccgacaa tagccccaag acgagaaagg tgaaaaacca      480
291   aaataggact cattgatact gagagagaag tagcgataat agaatcgtga acgatcaaac      540
292   taatagtaag cagtattcct gttatatcga gcatagtttt tattttgact tttaaaccag      600
293   ggaacccta acttggattg ggtagttcta ggatttttta tt                                     642
295 <210> SEQ ID NO: 12
296 <211> LENGTH: 582
297 <212> TYPE: DNA
298 <213> ORGANISM: Streptococcus pneumoniae
300 <400> SEQUENCE: 12
301   tacaattaac gaaataacta ataaaaccgg atgaactatc cgtcgtaagg tagaccgaat      60
302   taacaccggt tcgaacggtt tccttaacta taagccctcg tgccttcgcc gttgaatccg      120
303   cgatggttac gtaaggcatg taaccacatc tttcgaccaa gccagcagta tcggcctcta      180
304   taaaactttc cctgtgaccg ttgacgtaac ggaaaagagt acgtacaact ataagtgggc      240
305   gaagaacgtc ctcagaaaacg ccaaaatccg gtgcacaaag ggtagaagcg gtttaaattt      300
306   ccgccatttc ggcaccgtg tagtcctccg caaaacgata aaatgcgtgg ggacaataaa      360
307   tagtgctacc aacgccataa gaagtagaaa aatatgaact gatttaaaca aagagagagt      420
308   agctacaatt gtccctagat atgacaatat atatcaaaga aacagggtact atgcataaat      480
309   aactaacagc aatgggacga gtgataaaaa cactatatgt ctgtggctcg cttgtaattt      540
310   gcttaatagt tattttgtct tggatttcat tttaccaata tt                                     582
W--> 320 40021649.doc

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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10068080.txt

Output Set: N:\CRF3\02152002\J068080.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:14 M:280 W: Numeric Identifier already exists, <140> found multiple times
L:14 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:14 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:320 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12